

M. Walicka

#9
MP 3-8.01

1652

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/273,957

DATE: 03/08/2001
 TIME: 13:29:26

Input Set : A:\GC477C1-SEQLIST.txt
 Output Set: N:\CRF3\03082001\I273957.raw

P-5
ENTERED

3 <110> APPLICANT: Wang, Huaming
 4 Wang, Cynthia C.
 5 Amory, Antoine
 6 Dhaese, Patrick
 7 Lambrechts-Rongvaux, Annick
 9 <120> TITLE OF INVENTION: Novel Phenol Oxidizing Enzyme Enzymes
 11 <130> FILE REFERENCE: GC477C1
 13 <140> CURRENT APPLICATION NUMBER: US 09/273,957
 14 <141> CURRENT FILING DATE: 1999-03-22
 16 <160> NUMBER OF SEQ ID NOS: 14
 18 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1791
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Stachybotrys chartarum
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 27 ctccgcatcc cgatggacac cggcagccac cccattgagg ctgttgatcc cgaagtgaag 120
 28 actgaggtct tcgctgactc cctccttgct gcagcaggcg atgacgactg ggagtcacct 180
 29 ccatacaact tgcctttacag gaatgccctg ccaattccac ctgtcaagca gcccaagatg 240
 30 atcattacca accctgtcac cggcaaggac atttggtagt atgagatcga gatcaagcca 300
 31 tttcagcaaa ggattttacc cactttgcgc cctgccactc tcgtcggcta cgatggcatg 360
 32 agccctgggt ctactttcaa tgttccaga ggaacagaga ctgtagttag gttcatcaac 420
 33 aatgccaccg tggagaactc ggtccatctg caaggctccc catcgctgac ccctttcgat 480
 34 gggtgggctg aagatgtgac ctccctggc gagtacaagg attactactt tcccaactac 540
 35 caatccgccc gccttctgtg gtaccatgac cagcctttca tgaagactgc tgagaatgcc 600
 36 tactttgggt aggctggcgc ctacattatc aacgacgagg ctgaggatgc tctcggctct 660
 37 cctagtggct atggcgagtt cgatatccct ctgatcctga cggccaagta ctataacgcc 720
 38 gatgggtacc tgcgttcgac cgaagggtgag gaccaggacc tgtggggaga tgtcatccat 780
 39 gtcaacggac agccatggcc ttctcctaac gtccagcccc gcaagtaacc ttccgatcc 840
 40 ctcaacgctg ccgtgtctcg tgccttgctc ctctacctcg tcaggaccag ctctcccaac 900
 41 gtcagaattc ctttccaagt catctgctct gatgctggtc tccctcaagc ccccgctcag 960
 42 acctctaacc tctaccttgc tgttgccgag cyttacgaga tcattattga cttcaccaac 1020
 43 tttgctggcc agactcttga cctgcgcaac gttgctgaga ccaacgatgt cggcgacgag 1080
 44 gatgagtacg ctgcgactct cgaaggatg cgtctcgtcg tcagctctgg cactgttgag 1140
 45 gacaacagcc aggtccctc cactctccgt gacgttccct tccctcctca caaggaaagg 1200
 46 cccgccgaca agcacttcaa gtttgaacgc agcaacggac actacctgat caacgatgtt 1260
 47 ggccttgccg atgtcaatga gcgtgtcctg gcccaagccc agctcggcac cgttgaggtc 1320
 48 tgggagctcg agaactcctc tggaggctgg agccacccc tccacattca ccttggtgac 1380
 49 ttcaagatcc tcaagcgaa cgttggtcgt ggcagggtca tgcctacga gtcgtctggt 1440
 50 cttaaggatg tcgtctggtt gggcaggggg gagaccctga ccatcgaggc ccaactacaa 1500
 51 ccttgagctg gagcttacat gtggcactgt cacaacctca ttcacgagga taacgacatg 1560
 52 atggctgtat tcaacgtcac cggcatggag gagaagggat atcttcagga ggacttcgag 1620
 53 gaccccatga accccaagt ggcgcgcgtt ccttacaacc gcaacgactt ccatgctcgc 1680
 54 gctggaaact tctccgcca gtccatcact gcccgagtgc aggagctggc cgagcaggag 1740
 55 ccgtacaacc gcctcgatga gatcctggag gatcttgga tcgaggagta a 1791
 57 <210> SEQ ID NO: 2

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58 <211> LENGTH: 594
59 <212> TYPE: PRT
60 <213> ORGANISM: Stachybotrys chartarum
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66 20 25 30
67 Val Asp Pro Glu Val Lys Thr Glu Val Phe Ala Asp Ser Leu Leu Ala
68 35 40 45
69 Ala Ala Gly Asp Asp Asp Trp Glu Ser Pro Pro Tyr Asn Leu Leu Tyr
70 50 55 60
71 Arg Asn Ala Leu Pro Ile Pro Pro Val Lys Gln Pro Lys Met Ile Ile
72 65 70 75 80
73 Thr Asn Pro Val Thr Gly Lys Asp Ile Trp Tyr Tyr Glu Ile Glu Ile
74 85 90 95
75 Lys Pro Phe Gln Gln Arg Ile Tyr Pro Thr Leu Arg Pro Ala Thr Leu
76 100 105 110
77 Val Gly Tyr Asp Gly Met Ser Pro Gly Pro Thr Phe Asn Val Pro Arg
78 115 120 125
79 Gly Thr Glu Thr Val Val Arg Phe Ile Asn Asn Ala Thr Val Glu Asn
80 130 135 140
81 Ser Val His Leu His Gly Ser Pro Ser Arg Ala Pro Phe Asp Gly Trp
82 145 150 155 160
83 Ala Glu Asp Val Thr Phe Pro Gly Glu Tyr Lys Asp Tyr Tyr Phe Pro
84 165 170 175
85 Asn Tyr Gln Ser Ala Arg Leu Leu Trp Tyr His Asp His Ala Phe Met
86 180 185 190
87 Lys Thr Ala Glu Asn Ala Tyr Phe Gly Gln Ala Gly Ala Tyr Ile Ile
88 195 200 205
89 Asn Asp Glu Ala Glu Asp Ala Leu Gly Leu Pro Ser Gly Tyr Gly Glu
90 210 215 220
91 Phe Asp Ile Pro Leu Ile Leu Thr Ala Lys Tyr Tyr Asn Ala Asp Gly
92 225 230 235 240
93 Thr Leu Arg Ser Thr Glu Gly Glu Asp Gln Asp Leu Trp Gly Asp Val
94 245 250 255
95 Ile His Val Asn Gly Gln Pro Trp Pro Phe Leu Asn Val Gln Pro Arg
96 260 265 270
97 Lys Tyr Arg Phe Arg Phe Leu Asn Ala Ala Val Ser Arg Ala Trp Leu
98 275 280 285
99 Leu Tyr Leu Val Arg Thr Ser Ser Pro Asn Val Arg Ile Pro Phe Gln
100 290 295 300
101 Val Ile Ala Ser Asp Ala Gly Leu Leu Gln Ala Pro Val Gln Thr Ser
102 305 310 315 320
103 Asn Leu Tyr Leu Ala Val Ala Glu Arg Tyr Glu Ile Ile Ile Asp Phe
104 325 330 335
105 Thr Asn Phe Ala Gly Gln Thr Leu Asp Leu Arg Asn Val Ala Glu Thr
106 340 345 350
107 Asn Asp Val Gly Asp Glu Asp Glu Tyr Ala Arg Thr Leu Glu Val Met

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108          355          360          365
109 Arg Phe Val Val Ser Ser Gly Thr Val Glu Asp Asn Ser Gln Val Pro
110          370          375          380
111 Ser Thr Leu Arg Asp Val Pro Phe Pro Pro His Lys Glu Gly Pro Ala
112 385          390          395          400
113 Asp Lys His Phe Lys Phe Glu Arg Ser Asn Gly His Tyr Leu Ile Asn
114          405          410          415
115 Asp Val Gly Phe Ala Asp Val Asn Glu Arg Val Leu Ala Lys Pro Glu
116          420          425          430
117 Leu Gly Thr Val Glu Val Trp Glu Leu Glu Asn Ser Ser Gly Gly Trp
118          435          440          445
119 Ser His Pro Val His Ile His Leu Val Asp Phe Lys Ile Leu Lys Arg
120          450          455          460
121 Thr Gly Gly Arg Gly Gln Val Met Pro Tyr Glu Ser Ala Gly Leu Lys
122 465          470          475          480
123 Asp Val Val Trp Leu Gly Arg Gly Glu Thr Leu Thr Ile Glu Ala His
124          485          490          495
125 Tyr Gln Pro Trp Thr Gly Ala Tyr Met Trp His Cys His Asn Leu Ile
126          500          505          510
127 His Glu Asp Asn Asp Met Met Ala Val Phe Asn Val Thr Ala Met Glu
128          515          520          525
129 Glu Lys Gly Tyr Leu Gln Glu Asp Phe Glu Asp Pro Met Asn Pro Lys
130          530          535          540
131 Trp Arg Ala Val Pro Tyr Asn Arg Asn Asp Phe His Ala Arg Ala Gly
132 545          550          555          560
133 Asn Phe Ser Ala Glu Ser Ile Thr Ala Arg Val Gln Glu Leu Ala Glu
134          565          570          575
135 Gln Glu Pro Tyr Asn Arg Leu Asp Glu Ile Leu Glu Asp Leu Gly Ile
136          580          585          590
137 Glu Glu

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140 <210> SEQ ID NO: 3

141 <211> LENGTH: 3677

142 <212> TYPE: DNA

143 <213> ORGANISM: Stachybotrys chartarum

145 <400> SEQUENCE: 3

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147 agtcaatata ttggtcactg ctaatagtgc cttgtctacg gcaaaaagct ccttgccgaa      120
148 ggggcacaga ctatcaagtg agacataatg gatgcatgtc ttctatagcc acagttaggg      180
149 tgggtgaacta ctgaagagg ccccgacttg catgcatacg acatgtcgct tccatgcaac      240
150 atgtatgcgc acatcggcga tcaggcacc tctgcatgca gaatagaacc cccctgggtt      300
151 ccttttgttt cttttccttt ctcaacgacg cgtgagcgtg gtttaacttga gcaaggccga      360
152 gtggtctgtt cacyaggtta ccatcgaact ctcttctttc ccaatcatga cctgcccccc      420
153 gagtttagcc cccatcacgg ctgtgaaatc cacttcgata atcctagcct agtgctactc      480
154 ttcaatagtt gctcctgatg gggcactttg gtcacattgc cttgggttyct cctacctcgt      540
155 tctcttccgc atcaagcctc tatgcccac gacaacacct cattggcccg gaccactttg      600
156 agcgcgcacg cacttcgcg cgaaggagt tgataacacc cttcaccctt gcccaatgat      660
157 ggagtttttg tctatttgc atgatcacct cacattcact agatcacgga tccctggaaga      720
158 ggggtgtgaa gccagaccag cttgtccctg ttcttgacga ctacaggtcag ctccatagcg      780
159 ctatcacagc tcaggattat caagtccctt aaagtccaga cccttttcat tgtatgatgc      840

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160 tgcctaattt ggcgtatctc tatgcccgtag cagccgctct ggctacaact ggctgccatg 900
161 gctgaagcat cgtgagatct ataaaggctc ccgaatcctc ggtgaagtca gaatcgtctc 960
162 tccacaccag tcaacaacaa gcttctttct cttacagctt agcctqagca cattcacaga 1020
163 actcttccct tcttttcgtc aatatgtctg tcaagtcatt gcaactggca gcagcctccg 1080
164 ggctcctgtc tggagtcctc ggcattccga tggacaccgg cagccacccc attgaggctg 1140
165 ttgatcccg aagtgaagact gaggtcttct ctgactccct ccttctgtca gcaggcgatg 1200
166 acgactggga gtcacctcca tacaacttgc ttacaggtg agacacctgt cccacctgtt 1260
167 ttccctcgat aactaactct tatagjaatg cctggccaat tccacctgtc aagcagccca 1320
168 agatgtatgt ctttgatttt ctacgaagca actcggcccc gactaatgta ttctaggatc 1380
169 attaccaacc ctgtcaccgg caaggacatt tggtagctat agatcgagat caagccattt 1440
170 cagcaaaggg tgagtttgcg cagaaacctt gtggttaatta atcattgtta ctgacctttt 1500
171 cagatttacc ccaccttgcg cctgcgcaat cctgctggct acgatggcat gagccctggt 1560
172 cctactttca atgttcccg aggaucagag actgtagtta ggttcatcaa caatgccacc 1620
173 gtggagaact cgggtccatct gcacggctcc ccatcgctg cccctttcga tggttgggct 1680
174 gaagatgtga ccttccctgg cgagtacaag gattactact ttcccaacta ccaatccgcc 1740
175 cgccttctgt ggtaccatga ccacgctttc atgaaggatg gctacgagcc tttatcttct 1800
176 ttggtacact ttggttaacc aacttctttt cgtagactgc tgagaatgcc tactttggtc 1860
177 aggctggcgc ctacattatc aacgacgagg ctgaggatgc tctcggtctt cctagtggct 1920
178 atggcgagtt cgtatccctt ctgattcctga cggccaagta ctataacgcc gatggtaccc 1980
179 tgcgttcgac cgagggttag gaccaggacc tgtggggaga tgtcatccat gtcaacggac 2040
180 agccatggcc tttcttaacc gtccagcccc gcaagtaccg ttccgatctc ctcaacgctg 2100
181 ccgtgtctcg tgcctggctc ctctacctcg tcaggaccag ctctcccaac gtcaaatctc 2160
182 ctttcaaagt cattgctctt gatgtgggtc tcttcaagc ccccgttcag acctctaacc 2220
183 tctaccttgc tgttgcggag cgttacgaga tcattattgg tatgccctcc cctctcaaga 2280
184 atgagtcagg aactctaaga ctaacacttg tagacttcac caactttgct ggccagactc 2340
185 ttgacctgac caacgttgcg gagaccaacg atgtcgcgca cgaggatgag tacgctcgca 2400
186 ctctcgaggt gatgcgcttc gtcgtcagct ctggcactgt tgaggacaac agccagggtc 2460
187 cctccactct ccgtgacgtt cctttccctc ctcaacaagg aggccccgcc gacaagcact 2520
188 tcaagtttga acgcagcaac ggaactacc tgatcaacga tgttggcttt gccgatgtca 2580
189 atgagcgtgt cctggccaag cccgagctcg gcaccgttga ggtctgggag ctcgagaact 2640
190 cctctggagg ctggagccac cccgtccaca ttacacttgt tgacttcaag atcctcaagc 2700
191 gaactggtgg tctggtccag gtcattgccc acgagtcctc tggctttaag gatgtcgtct 2760
192 ggttgggagc ggtgagacc ctgacctcg agggccacta ccaacctgg actggagctt 2820
193 acatgtggca ctgtcacacc ctcatcacc aggataacga catgatggct gtattcaacg 2880
194 tcaccgccat gtagggagaag ggatactctc aggaggactt cgaggacccc atgaaccca 2940
195 agtggcgccg cgttccctac aaccgcaacg acttccatgc tgcgctgga aacttctccg 3000
196 ccgagtcctt cactgcccga gtgcaggagc tggccgagca ggagccgtac aaccgcctcg 3060
197 atgagatcct gtagggtctt ggaatcgagg agtaaacccc gagccacaag ctctacaatc 3120
198 gttttgagtc ttaagacgag gctcttggty cgtattcttt tcttccctac ggggaactcc 3180
199 gctgtccact gcgatgtgaa ggaccatcac aaagcaacgt atattattga ctaccactg 3240
200 tcattaccgc ccacttgtac ctattcgatt cttgttcaaa cttttctagt gcgagagtg 3300
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204 aaggttgaga atgcattcga cggaaatcatt tgatgctctc agctcgattt accgatgtaa 3540
205 gacaagttag gtaagtgtct tggatatccga aatgactca ggctccctca ttaggttyca 3600
206 tgtgaaaacc ttacgcaact catgggtgtt gggaccaaata catccatacc tgattttgat 3660
207 aactgacctg ggtcaat 3677
209 <210> SEQ ID NO: 4

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210 <211> LENGTH: 572
211 <212> TYPE: PRT
212 <213> ORGANISM: Myrothecium Verrucaria
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218 20 25 30
219 Gly His Leu Phe Lys Arg Val Ala Gln Ile Ser Pro Gln Tyr Pro Met
220 35 40 45
221 Phe Thr Val Pro Leu Pro Ile Pro Pro Val Lys Gln Pro Arg Leu Thr
222 50 55 60
223 Val Thr Asn Pro Val Asn Gly Gln Glu Ile Trp Tyr Tyr Glu Val Glu
224 65 70 75 80
225 Ile Lys Pro Phe Thr His Gln Val Tyr Pro Asp Leu Gly Ser Ala Asp
226 85 90 95
227 Leu Val Gly Tyr Asp Gly Met Ser Pro Gly Pro Thr Phe Gln Val Pro
228 100 105 110
229 Arg Gly Val Glu Thr Val Val Arg Phe Ile Asn Asn Ala Glu Ala Pro
230 115 120 125
231 Asn Ser Val His Leu His Gly Ser Phe Ser Arg Ala Ala Phe Asp Gly
232 130 135 140
233 Trp Ala Glu Asp Ile Thr Glu Pro Gly Ser Phe Lys Asp Tyr Tyr Tyr
234 145 150 155 160
235 Pro Asn Arg Gln Ser Ala Arg Thr Leu Trp Tyr His Asp His Ala Met
236 165 170 175
237 His Ile Thr Ala Glu Asn Ala Tyr Arg Gly Gln Ala Gly Leu Tyr Met
238 180 185 190
239 Leu Thr Asp Pro Ala Glu Asp Ala Leu Asn Leu Pro Ser Gly Tyr Gly
240 195 200 205
241 Glu Phe Asp Ile Pro Met Ile Leu Thr Ser Lys Gln Tyr Thr Ala Asn
242 210 215 220
243 Gly Asn Leu Val Thr Thr Asn Gly Glu Leu Asn Ser Phe Trp Gly Asp
244 225 230 235 240
245 Val Ile His Val Asn Gly Gln Pro Trp Pro Phe Lys Asn Val Glu Pro
246 245 250 255
247 Arg Lys Tyr Arg Phe Arg Phe Leu Asp Ala Ala Val Ser Arg Ser Phe
248 260 265 270
249 Gly Leu Tyr Phe Ala Asp Thr Asp Ala Ile Asp Thr Arg Leu Pro Phe
250 275 280 285
251 Lys Val Ile Ala Ser Asp Ser Gly Leu Leu Glu His Pro Ala Asp Thr
252 290 295 300
253 Ser Leu Leu Tyr Ile Ser Met Ala Glu Arg Tyr Glu Val Val Phe Asp
254 305 310 315 320
255 Phe Ser Asp Tyr Ala Gly Lys Thr Ile Glu Leu Arg Asn Leu Gly Gly
256 325 330 335
257 Ser Ile Gly Gly Ile Gly Thr Asp Thr Asp Tyr Asp Asn Thr Asp Lys
258 340 345 350
259 Val Met Arg Phe Val Val Ala Asp Asp Thr Thr Gln Pro Asp Thr Ser

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FSI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10